

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/539,535A
Source: IFWP
Date Processed by STIC: 10/12/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/539,535A

TIME: 09:28:07

Input Set : A:\41384.txt

Output Set: N:\CRF4\10122006\J539535A.raw

3 <110> APPLICANT: Kloting, et al.

5 <120> TITLE OF INVENTION: Use of the Multifunctional Transcription Factor
Yin Yang 1 and

6 Variants Thereof for Treating Illnesses, Especially Type I

7 Diabetes

9 <130> FILE REFERENCE: 30572/41384

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,535A

C--> 11 <141> CURRENT FILING DATE: 2005-06-17

11 <150> PRIOR APPLICATION NUMBER: PCT/EP03/014762

12 <151> PRIOR FILING DATE: 2003-12-19

14 <150> PRIOR APPLICATION NUMBER: DE 102 61 650.7

15 <151> PRIOR FILING DATE: 2002-12-20

17 <160> NUMBER OF SEQ ID NOS: 232

19 <170> SOFTWARE: PatentIn version 3.3

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 2256

23 <212> TYPE: DNA

24 <213> ORGANISM: Rattus norv.

26 <220> FEATURE:

27 <221> NAME/KEY: Promoter

28 <222> LOCATION: (1)..(72)

30 <220> FEATURE:

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (73)..(1125)

33 <223> OTHER INFORMATION: YY1 (BB/OK)

35 <220> FEATURE:

36 <221> NAME/KEY: misc_feature

37 <222> LOCATION: (955)..(1125)

38 <223> OTHER INFORMATION: Zinc finger

40 <220> FEATURE:

41 <221> NAME/KEY: Intron

42 <222> LOCATION: (1126)..(1758)

44 <220> FEATURE:

45 <221> NAME/KEY: misc_feature

46 <222> LOCATION: (1759)..(1917)

47 <223> OTHER INFORMATION: Zinc finger

49 <220> FEATURE:

50 <221> NAME/KEY: CDS

51 <222> LOCATION: (1759)..(1938)

52 <223> OTHER INFORMATION: YY1 (BB/OK)

54 <400> SEQUENCE: 1

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57 gagccctcag cc atg gcc tcg ggc gac acc ctc tac att gcc acg gac ggc 111

58 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly

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59				1			5			10							
61	tcg	gag	atg	cca	gcc	gag	atc	gtg	gaa	ctg	cat	gag	att	gag	gtg	gag	159
62	Ser	Glu	Met	Pro	Ala	Glu	Ile	Val	Glu	Leu	His	Glu	Ile	Glu	Val	Glu	
63	15						20					25					
65	acc	atc	ccg	gtg	gag	act	atc	gag	acc	acg	gtg	gtg	ggc	gag	gag	gag	207
66	Thr	Ile	Pro	Val	Glu	Thr	Ile	Glu	Thr	Thr	Val	Val	Gly	Glu	Glu	Glu	
67	30						35				40					45	
69	gac	gac	gac	gaa	gac	gac	gag	gat	ggg	ggc	ggc	gga	gac	cac	ggg	ggc	255
70	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Gly	Gly	Gly	Asp	His	Gly	Gly	
71					50					55					60		
73	ggg	ggc	ggc	cac	ggg	cac	gct	ggc	cac	cac	cat	cac	cac	cac	cac	cac	303
74	Gly	Gly	Gly	His	Gly	His	Ala	Gly	His	His	His	His	His	His	His	His	
75				65					70				75				
77	cac	cac	ccg	ccc	atg	atc	gcg	ctg	cag	ccg	ctg	gtc	acc	gac	gac	ccg	351
78	His	His	Pro	Pro	Met	Ile	Ala	Gln	Pro	Leu	Val	Thr	Asp	Asp	Pro		
79			80					85				90					
81	acc	caa	gtg	cac	cac	cac	caa	gag	gtg	att	ctg	gtg	cag	acg	cgc	gag	399
82	Thr	Gln	Val	His	His	His	Gln	Glu	Val	Ile	Leu	Val	Gln	Thr	Arg	Glu	
83		95					100					105					
85	gag	gta	gtg	ggg	ggc	gac	gac	tcg	gac	ggg	ctg	cgc	gcc	gag	gac	ggg	447
86	Glu	Val	Val	Gly	Gly	Asp	Asp	Ser	Asp	Gly	Leu	Arg	Ala	Glu	Asp	Gly	
87	110					115					120					125	
89	ttc	gag	gac	cag	atc	ctc	att	ccg	gta	ccc	gcg	ccg	gcc	ggc	gga	gac	495
90	Phe	Glu	Asp	Gln	Ile	Leu	Ile	Pro	Val	Pro	Ala	Pro	Ala	Gly	Gly	Asp	
91					130					135					140		
93	gac	gac	tac	atc	gag	cag	acg	ctg	gtc	acc	gtg	gcg	gcg	gcc	ggc	aag	543
94	Asp	Asp	Tyr	Ile	Glu	Gln	Thr	Leu	Val	Thr	Val	Ala	Ala	Ala	Gly	Lys	
95				145					150				155				
97	agc	ggg	ggc	ggg	tct	tcg	tcg	ggc	ggc	ggc	cgc	gtt	aag	aag	ggc	ggc	591
98	Ser	Gly	Gly	Gly	Ser	Ser	Ser	Gly	Gly	Gly	Arg	Val	Lys	Lys	Gly	Gly	
99			160					165				170					
101	ggc	aag	aag	agc	ggc	aag	aag	agt	tac	ctg	ggc	agc	ggg	gcc	ggc	gcg	639
102	Gly	Lys	Lys	Ser	Gly	Lys	Lys	Ser	Tyr	Leu	Gly	Ser	Gly	Ala	Gly	Ala	
103		175					180					185					
105	gcg	ggc	ggg	ggc	ggc	gcc	gac	ccg	ggg	aat	aag	aag	tgg	gaa	cag	aag	687
106	Ala	Gly	Gly	Gly	Gly	Ala	Asp	Pro	Gly	Asn	Lys	Lys	Trp	Glu	Gln	Lys	
107	190					195					200						

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125 ccc aag caa ctg gca gaa ttt gcc aga atg aag cca aga aaa att aaa      927
126 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
127 270                               275                               280                               285
129 gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca      975
130 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
131                               290                               295                               300
133 aag atg ttc agg gat aac tct gct atg aga aag cat ctg cac acc cac      1023
134 Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
135                               305                               310                               315
137 ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gcg ttc gtt gag      1071
138 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
139                               320                               325                               330
141 agc tca aag cta aaa cga cac cag ctg gtt cat act gga gaa aag ccc      1119
142 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
143                               335                               340                               345
145 ttt cag gtagagccag ttcctgttcc ccaaactgca agctaggggtg ctggtcaggg      1175
146 Phe Gln
147 350
149 tggttgatat caagcactat ggggcaccgg ttgggggtatt ttattcccat ccctcctgtc      1235
151 tgcttggtt cctggttact gctcgggact gcagggtgta cagatggggg tggagggtt      1295
153 atgcgaagca ccccccact aaatttctag cagggtttaca aaaactcaac agttttgttt      1355
155 tgtagttagt agtgtgttga attactgata gagtgcctat aagtgcgtgt ggctacagct      1415
157 ccaggtgaca cttggtgctg cttatagaag actcgtgagt tgacagttgg catcactaaa      1475
159 tatcttaatc atctgtagtc tacttcctag agtgtctctg aaaacactca agctgtaaat      1535
161 ttgcactcag cacagccctt ctgtttctca agaactagcc atgggttgtt agtatcagag      1595
163 atcccagtgt gtcagttcta aaataccctc agaagggttc cagacgagga aggaggcatg      1655
165 ctccagcagaa tagtaggtgg tttccatcta agcagtgagc catcgatccc caggttctgg      1715
167 tctcatttgc caagagggtt gatattctggt ttttccttga cag tgc aca ttc gaa      1770
168                               Cys Thr Phe Glu
169                               355
171 ggc tgc ggg aag cgc ttt tca ctg gac ttc aat ttg cgc acg cat gtg      1818
172 Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg Thr His Val
173                               360                               365                               370
175 cga atc cat acc gga gac agg ccc tat gtg tgc ccc ttc gac ggt tgt      1866
176 Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe Asp Gly Cys
177                               375                               380                               385
179 aat aag aag ttt gct cag tca act aac ctg aaa tct cac atc tta aca      1914
180 Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His Ile Leu Thr
181                               390                               395                               400
183 cac gct aaa gcc aaa aac aac cag tgaaaagaag agagaagacc ttctcgaccc      1968
184 His Ala Lys Ala Lys Asn Asn Gln
185                               405                               410
187 cggaagcct cttcaggagt gtgattggga ataaatatgc ctctcctttg tatattatatt      2028
189 ctagggaagaa ttttaaaaat gaatcctaca cacttaagggt acatgttttg ataaagtagt      2088
191 aaaaatttaa aaaaatactt taataagatg acattgctaa gatgctctat ctgctctgt      2148
193 aatctcgttt caaaaacaag gtgtttttgt aaagtgtggc cccaacagga ggacaattca      2208
195 tgaacttcgc atcaaaagac aattctttat acaacagtgc taaaaatg      2256
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 411

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200 <212> TYPE: PRT
201 <213> ORGANISM: Rattus norv.
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (955)..(1125)
207 <223> OTHER INFORMATION: Zinc finger
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: (1759)..(1917)
212 <223> OTHER INFORMATION: Zinc finger
214 <400> SEQUENCE: 2
216 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met
217 1 5 10 15
220 Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
221 20 25 30
224 Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Asp Asp Asp
225 35 40 45
228 Glu Asp Asp Glu Asp Gly Gly Gly Asp His Gly Gly Gly Gly Gly
229 50 55 60
232 His Gly His Ala Gly His His His His His His His His His Pro
233 65 70 75 80
236 Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln Val
237 85 90 95
240 His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val Val
241 100 105 110
244 Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu Asp
245 115 120 125
248 Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp Tyr
249 130 135 140
252 Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly Gly
253 145 150 155 160
256 Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly Gly Lys Lys
257 165 170 175
260 Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala Ala Gly Gly
261 180 185 190
264 Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys Gln Val Gln
265 195 200 205
268 Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp Ser Ser Asp
269 210 215 220
272 Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu Gln Ile Ile
273 225 230 235 240
276 Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr Gly Lys Lys
277 245 250 255
280 Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp Pro Lys Gln
281 260 265 270
284 Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys Glu Asp Asp
285 275 280 285
288 Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr Lys Met Phe
289 290 295 300

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292 Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His Gly Pro Arg
293 305                               310                               315                               320
296 Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys
297                               325                               330                               335
300 Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys
301                               340                               345                               350
304 Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg
305                               355                               360                               365
308 Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe
309                               370                               375                               380
312 Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His
313 385                               390                               395                               400
316 Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
317                               405                               410
320 <210> SEQ ID NO: 3
321 <211> LENGTH: 2256
322 <212> TYPE: DNA
323 <213> ORGANISM: Rattus norv.
325 <220> FEATURE:
326 <221> NAME/KEY: Promoter
327 <222> LOCATION: (1)..(72)
329 <220> FEATURE:
330 <221> NAME/KEY: CDS
331 <222> LOCATION: (73)..(1125)
332 <223> OTHER INFORMATION: YY1 (SHR)
334 <220> FEATURE:
335 <221> NAME/KEY: misc_feature
336 <222> LOCATION: (955)..(1125)
337 <223> OTHER INFORMATION: Zinc finger
339 <220> FEATURE:
340 <221> NAME/KEY: Intron
341 <222> LOCATION: (1126)..(1758)
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (1759)..(1917)
346 <223> OTHER INFORMATION: Zinc finger
348 <220> FEATURE:
349 <221> NAME/KEY: CDS
350 <222> LOCATION: (1759)..(1938)
351 <223> OTHER INFORMATION: YY1 (SHR)
353 <400> SEQUENCE: 3
354 ccgcctcctc gccgcctc ccgcagccca ggagccgagg ctgccgcggc cgtggcgggc 60
355 gagccctcag cc atg gcc tcg ggc gac acc ctc tac att gcc acg gac ggc 111
357 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly
358 1 5 10
360 tcg gag atg cca gcc gag atc gtg gaa ctg cat gag att gag gtg gag 159
361 Ser Glu Met Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu
362 15 20 25
364 acc atc ccg gtg gag act atc gag acc acg gtg gtg ggc gag gag gag 207

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,535A

DATE: 10/12/2006

TIME: 09:28:08

Input Set : A:\41384.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date